SEQUENCE LISTING

(1) GENERAL INFORMATION:

   (i) APPLICANT: O'BRIEN, JOHN S.
            KISHIMOTO, YASUO

  (ii) TITLE OF INVENTION: IDENTIFICATION OF PROSAPOSIN AS A
      NEUROTROPHIC FACTOR

 (iii) NUMBER OF SEQUENCES: 4

  (iv) CORRESPONDENCE ADDRESS:
      (A) ADDRESSEE: KNOBBE, MARTENS, OLSON AND BEAR
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      (C) CITY: NEWPORT BEACH
      (D) STATE: CA
      (E) COUNTRY: USA
      (F) ZIP: 92660

   (v) COMPUTER READABLE FORM:
      (A) MEDIUM TYPE: Floppy disk
      (B) COMPUTER: IBM PC compatible
      (C) OPERATING SYSTEM: PC-DOS/MS-DOS
      (D) SOFTWARE: PatentIn Release #1.0, Version #1.25

  (vi) CURRENT APPLICATION DATA:
      (A) APPLICATION NUMBER:
      (B) FILING DATE:
      (C) CLASSIFICATION:

 (viii) ATTORNEY/AGENT INFORMATION:
      (A) NAME: Israelsen, Ned A.
      (B) REGISTRATION NUMBER: 29,655
      (C) REFERENCE/DOCKET NUMBER: OBRIEN.002A

  (ix) TELECOMMUNICATION INFORMATION:
      (A) TELEPHONE: 619-235-8550
      (B) TELEFAX: 619-235-0176

(2) INFORMATION FOR SEQ ID NO:1:

   (i) SEQUENCE CHARACTERISTICS:
      (A) LENGTH: 22 amino acids
      (B) TYPE: amino acid
      (C) STRANDEDNESS: single
      (D) TOPOLOGY: linear

  (ii) MOLECULE TYPE: peptide

 (iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

    (v) FRAGMENT TYPE: internal

(vii) IMMEDIATE SOURCE:
      (B) CLONE: 22-MER FRAGMENT

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

    Cys Glu Phe Leu Val Lys Glu Val Thr Lys Leu Ile Asp Asn Asn Lys
    1   5   10   15

    Thr Glu Lys Glu Ile Leu
                20

(2) INFORMATION FOR SEQ ID NO:2:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 523 amino acids
        (B) TYPE: amino acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: peptide

    (iii) HYPOTHETICAL: NO

    (iv) ANTI-SENSE: NO

    (v) FRAGMENT TYPE: N-terminal

(vii) IMMEDIATE SOURCE:
      (B) CLONE: PROSAPOSIN

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

    Met Tyr Ala Leu Phe Leu Leu Ala Ser Leu Leu Gly Ala Ala Leu Ala
    1   5   10   15

    Gly Pro Val Leu Gly Leu Lys Glu Cys Thr Arg Gly Ser Ala Val Trp
                20   25   30

    Cys Gln Asn Val Lys Thr Ala Ser Asp Cys Gly Ala Val Lys His Cys
                35   40   45

    Leu Gln Thr Val Trp Asn Lys Pro Thr Val Lys Ser Leu Pro Cys Asp
        50   55   60

    Ile Cys Lys Asp Val Val Thr Ala Ala Gly Asp Met Leu Lys Asp Asn
    65   70   75   80

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Ala Thr Glu Glu Glu Ile Leu Val Tyr Leu Glu Lys Thr Cys Asp Trp
                    85   90   95

Leu Pro Lys Pro Asn Met Ser Ala Ser Cys Lys Glu Ile Val Asp Ser
                100   105   110

Tyr Leu Pro Val Ile Leu Asp Ile Ile Lys Gly Glu Met Ser Arg Pro
                115   120   125

Gly Glu Val Cys Ser Ala Leu Asn Leu Cys Glu Ser Leu Gln Lys His
    130   135   140

Leu Ala Glu Leu Asn His Gln Lys Gln Leu Glu Ser Asn Lys Ile Pro
145   150   155   160

Glu Leu Asp Met Thr Glu Val Val Ala Pro Phe Met Ala Asn Ile Pro
                165   170   175

Leu Leu Leu Tyr Pro Gln Asp Gly Pro Arg Ser Lys Pro Gln Pro Lys
                180   185   190

Asp Gly Asp Val Cys Gln Asp Cys Ile Gln Met Val Thr Asp Ile Gln
    195   200   205

Thr Ala Val Arg Thr Asn Ser Thr Phe Val Gln Ala Leu Val Glu His
    210   215   220

Val Lys Glu Glu Cys Asp Arg Leu Gly Pro Gly Met Ala Asp Ile Cys
225   230   235   240

Lys Asn Tyr Ile Ser Gln Tyr Ser Glu Ile Ala Ile Gln Met Met Met
                245   250   255

His Met Gln Pro Lys Glu Ile Cys Ala Leu Val Gly Phe Cys Asp Glu
            260   265   270

Val Lys Glu Met Pro Met Gln Thr Leu Val Pro Ala Lys Val Ala Ser
    275   280   285

Lys Asn Val Ile Pro Ala Leu Asp Leu Val Asp Pro Ile Lys Lys His
    290   295   300

Glu Val Pro Ala Lys Ser Asp Val Tyr Cys Glu Val Cys Glu Phe Leu
305   310   315   320

Val Lys Glu Val Thr Lys Leu Ile Asp Asn Asn Lys Thr Glu Lys Glu
            325   330   335

Ile Leu Asp Ala Phe Asp Lys Met Cys Ser Lys Leu Pro Lys Ser Leu
            340   345   350

Ser Glu Glu Cys Gln Glu Val Val Asp Thr Tyr Gly Ser Ser Ile Leu
    355   360   365

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Ser Ile Leu Leu Glu Glu Val Ser Pro Glu Leu Val Cys Ser Met Leu
    370             375             380
His Leu Cys Ser Gly Thr Arg Leu Pro Ala Leu Thr Val His Val Thr
385             390             395             400
Gln Pro Lys Asp Gly Gly Phe Cys Glu Val Cys Lys Lys Leu Val Gly
            405             410             415
Tyr Leu Asp Arg Asn Leu Glu Lys Asn Ser Thr Lys Gln Glu Ile Leu
            420             425             430
Ala Ala Leu Glu Lys Gly Cys Ser Phe Leu Pro Asp Pro Tyr Gln Lys
        435             440             445
Gln Cys Asp Gln Phe Val Ala Glu Tyr Glu Pro Val Leu Ile Glu Ile
    450             455             460
Leu Val Glu Val Met Asp Pro Ser Phe Val Cys Leu Lys Ile Gly Ala
465             470             475             480
Cys Pro Ser Ala His Lys Pro Leu Leu Gly Thr Glu Lys Cys Ile Trp
            485             490             495
Gly Pro Ser Tyr Trp Cys Gln Asn Thr Glu Thr Ala Ala Gln Cys Asn
            500             505             510
Ala Val Glu His Cys Lys Arg His Val Trp Asn
        515             520
```

(2) INFORMATION FOR SEQ ID NO:3:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 80 amino acids
        (B) TYPE: amino acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: protein

    (iii) HYPOTHETICAL: NO

    (iv) ANTI-SENSE: NO

    (v) FRAGMENT TYPE: internal

    (vii) IMMEDIATE SOURCE:
        (B) CLONE: SAPOSIN C

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

```
Ser Asp Val Tyr Cys Glu Val Cys Glu Phe Leu Val Lys Glu Val Thr
1               5               10              15
```

```
Lys Leu Ile Asp Asn Asn Lys Thr Glu Lys Glu Ile Leu Asp Ala Phe
            20                25                30
Asp Lys Met Cys Ser Lys Leu Pro Lys Ser Leu Ser Glu Glu Cys Gln
            35                40                45
Glu Val Val Asp Thr Tyr Gly Ser Ser Ile Leu Ser Ile Leu Leu Glu
            50                55                60
Glu Val Ser Pro Glu Leu Val Cys Ser Met Leu His Leu Cys Ser Gly
    65                70                75                80
```

(2) INFORMATION FOR SEQ ID NO:4:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 2740 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: cDNA

    (iii) HYPOTHETICAL: NO

    (iv) ANTI-SENSE: NO

    (vii) IMMEDIATE SOURCE:
        (B) CLONE: PROSAPOSIN cDNA

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

```
ATGTACGCCC TCTTCCTCCT GGCCAGCCTC CTGGGCGCGG CTCTAGCCGG CCCGGTCCTT      60
GGACTGAAAG AATGCACCAG GGGCTCGGCA GTGTGGTGCC AGAATGTGAA GACGGCGTCC     120
GACTGCGGGG CAGTGAAGCA CTGCCTGCAG ACCGTTTGGA ACAAGCCAAC AGTGAAATCC     180
CTTCCCTGCG ACATATGCAA AGACGTTGTC ACCGCAGCTG GTGATATGCT GAAGGACAAT     240
GCCACTGAGG AGGAGATCCT TGTTTACTTG GAGAAGACCT GTGACTGGCT TCCGAAACCG     300
AACATGTCTG CTTCATGCAA GGAGATAGTG GACTCCTACC TCCCTGTCAT CCTGGACATC     360
ATTAAAGGAG AAATGAGCCG TCCTGGGGAG GTGTGCTCTG CTCTCAACCT CTGCGAGTCT     420
CTCCAGAAGC ACCTAGCAGA GCTGAATCAC CAGAAGCAGC TGGAGTCCAA TAAGATCCCA     480
GAGCTGGACA TGACTGAGGT GGTGGCCCCC TTCATGGCCA ACATCCCTCT CCTCCTCTAC     540
CCTCAGGACG GCCCCCGCAG CAAGCCCCAG CCAAAGGATA ATGGGGACGT TTGCCAGGAC     600
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TGCATTCAGA TGGTGACTGA CATCCAGACT GCTGTACGGA CCAACTCCAC CTTTGTCCAG   660

GCCTTGGTGG AACATGTCAA GGAGGAGTGT GACCGCCTGG GCCCTGGCAT GGCCGACATA   720

TGCAAGAACT ATATCAGCCA GTATTCTGAA ATTGCTATCC AGATGATGAT GCACATGCAA   780

CCCAAGGAGA TCTGTGCGCT GGTTGGGTTC TGTGATGAGG TGAAAGAGAT GCCCATGCAG   840

ACTCTGGTCC CCGCCAAAGT GGCCTCCAAG AATGTCATCC CTGCCCTGGA ACTGGTGGAG   900

CCCATTAAGA AGCACGAGGT CCCAGCAAAG TCTGATGTTT ACTGTGAGGT GTGTGAATTC   960

CTGGTGAAGG AGGTGACCAA GCTGATTGAC AACAACAAGA CTGAGAAAGA AATACTCGAC   1020

GCTTTTGACA AAATGTGCTC GAAGCTGCCG AAGTCCCTGT CGGAAGAGTG CCAGGAGGTG   1080

GTGGACACGT ACGGCAGCTC CATCCTGTCC ATCCTGCTGG AGGAGGTCAG CCCTGAGCTG   1140

GTGTGCAGCA TGCTGCACCT CTGCTCTGGC ACGCGGCTGC CTGCACTGAC CGTTCACGTG   1200

ACTCAGCCAA AGGACGGTGG CTTCTGCGAA GTGTGCAAGA AGCTGGTGGG TTATTTGGAT   1260

CGCAACCTGG AGAAAAACAG CACCAAGCAG GAGATCCTGG CTGCTCTTGA GAAAGGCTGC   1320

AGCTTCCTGC CAGACCCTTA CCAGAAGCAG TGTGATCAGT TTGTGGCAGA GTACGAGCCC   1380

GTGCTGATCG AGATCCTGGT GGAGGTGATG GATCCTTCCT TCGTGTGCTT GAAAATTGGA   1440

GCCTGCCCCT CGGCCCATAA GCCCTTGTTG GGAACTGAGA AGTGTATATG GGGCCCAAGC   1500

TACTGGTGCC AGAACACAGA GACAGCAGCC CAGTGCAATG CTGTCGAGCA TTGCAAACGC   1560

CATGTGTGGA ACTAGGAGGA GGAATATTCC ATCTTGGCAG AAAGCACAGC ATTGGTTTTT   1620

TTCTACTTGT GTGTCTGGGG GAATGAACGC ACAGATCTGT TTGACTTTGT TATAAAAATA   1680

GGGCTCCCCC ACCTCCCCCA TTTCTGTGTC CTTTATTGTA GCATTGCTGT CTGCAAGGGA   1740

GCCCCTAGCC CCTGGCAGAC ATAGCTGCTT CAGTGCCCCT TTTCTGTCTG CTAGATGGAT   1800

GTTGATGCAC TGGAGGTCTT TTAGCCTGCC CTTGCATGGC GCCTGCTGGA GGAGGAGAGA   1860

GCTCTGCTGG CATGAGCCAC AGTTTCTTGA CTGGAGGCCA TCAACCCTCT TGGTTGAGGC   1920

CTTGTTCTGA GCCCTGACAT GTGCTTGGGC ACTGGTGGGC CTGGGCTTCT GAGGTGGCCT   1980

CCTGCCCTGA TCAGGGACCC TCCCCGCTTT CCTGGGCCTC TCAGTTGAAC AAAGCAGCAA   2040

AACAAAGGCA GTTTTATATG AAAGATTAGA AGCCTGGAAT AATCAGGCTT TTTAAATGAT   2100

GTAATTCCCA CTGTAATAGC ATAGGGATTT TGGAAGCAGC TGCTGGTGGC TTGGGACATC   2160

AGTGGGGCCA AGGGTTCTCT GTCCCTGGTT CAACTGTGAT TTGGCTTTCC CGTGTCTTTC   2220

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CTGGTGATGC CTTGTTTGGG GTTCTGTGGG TTTGGGTGGG AAGAGGGCAA TCTGCCTGAA   2280

TGTAACCTGC TAGCTCTCCG AAGGCCCTGC GGGCCTGGCT TGTGTGAGCG TGTGGACAGT   2340

GGTGGCCGCG CTGTGCCTGC TCGTGTTGCC TACATGTCCC TGGCTGTTGA GGCGCTGCTT   2400

CAGCCTGCAC CCCTCCCTTG TCTCATAGAT GCTCCTTTTG ACCTTTTCAA ATAAATATGG   2460

ATGGCGAGCT CCTAGGCCTC TGGCTTCCTG GTAGAGGGCG GCATGCCGAA GGGTCTGCTG   2520

GGTGTGGATT GGATGCTGGG GTGTGGGGGT TGGAAGCTGT CTGTGGCCCA CTTGGGCACC   2580

CACGCTTCTG TCCACTTCTG GTTGCCAGGA GACAGCAAGC AAAGCCAGCA GGACATGAAG   2640

TTGCTATTAA ATGGACTTCG TGATTTTTGT TTTGCACTAA AGTTTCTGTG ATTTAACAAT   2700

AAAATTCTGT TAGCCAGAAA AAAAAAAAAA AAAAAAAAAA   2740

(2) INFORMATION FOR SEQ ID NO:5:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 18 amino acids
        (B) TYPE: amino acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

   (ii) MOLECULE TYPE: peptide

  (iii) HYPOTHETICAL: NO

   (iv) ANTISENSE: NO

    (v) FRAGMENT TYPE: internal

  (vii) IMMEDIATE SOURCE:
        (B) CLONE: 18-MER FRAGMENT

   (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5

Tyr Lys Glu Val Thr Lys Leu Ile Asp Asn Asn Lys Thr Glu Lys Glu
1   5   10   15

Ile Leu

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